

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:25:32 ; Search time 6.69697 Seconds  
(without alignments)  
91.287 Million cell updates/sec

Title: US-09-743-225-10  
Perfect score: 66  
Sequence: 1 CATLRVYKGGXA 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	59.1	239	1 RPIA_CHLMU	Q9pk10 chlamydia m
2	38	57.6	405	1 PE21_MOUSE	P35375 mus musculus
3	38	57.6	405	1 BACC_BACLI	O68008 b bacitraci
4	37	56.1	1435	1 TR85_HUMAN	Q9v215 homo sapien
5	36	54.5	367	1 INK4_DROME	Q9vrx6 drosophila
6	35	53.0	231	1 RPIA_AGRF5	Q8ue20 agrobacteri
7	35	53.0	231	1 RPIA_CHLPN	Q92942 chlamydia p
8	35	53.0	231	1 RPIA_RHIME	Q92pb8 rhizobium m
9	35	53.0	234	1 RPIA_METAC	O8tg69 methanosarc
10	35	53.0	242	1 RPIA_CHLTR	O84215 chlamydia t
11	35	53.0	244	1 PHOS_MOUSE	Q9gw08 mus musculus
12	35	53.0	245	1 PHOS_BOVIN	P15632 bos taurus
13	35	53.0	245	1 PHOS_FELCA	P41686 felis silve
14	35	53.0	246	1 PHOS_RAT	P20942 rattus norv
15	35	53.0	340	1 CFPA_BACUT	Q45729 bacillus th
16	35	53.0	424	1 VGLI_HSVB3	P18553 equine herp
17	35	53.0	712	1 CDGT_BACS3	P09121 bacillus sp
18	35	53.0	713	1 AMYR_BACS8	P17692 bacillus sp
19	35	53.0	713	1 CDGT_BACS0	P05618 bacillus sp
20	35	53.0	713	1 CDGT_BACPS	P030921 bacillus sp
21	35	53.0	713	1 CDGU_BACCI	P43379 bacillus ci
22	34	51.5	110	1 THIO_STRCO	P52230 streptomyce
23	34	51.5	215	1 SC2_OCTDO	P27010 octopus dof
24	34	51.5	245	1 PHOS_CANPA	O77560 canis famli
25	34	51.5	246	1 PHOS_HUMAN	P20941 homo sapien
26	34	51.5	246	1 VMTV_LAMB2	P03733 bacterioph
27	34	51.5	327	1 DRN1_STREQ	P26295 streptococc
28	34	51.5	345	1 APDH_HUMAN	P03749 homo sapien
29	34	51.5	349	1 ADH1_ASPTL	P41747 aspergillus
30	34	51.5	349	1 ADH1_EMENT	P08843 emericeila
31	34	51.5	349	1 RADA_PYRFO	O74036 pyrococcus
32	34	51.5	352	1 ADH3_EMENT	P07754 emericeila
33	34	51.5	353	1 ADH1_NEUCR	Q9p6c8 neurospora

34	51.5	356	1 RADA_PYRAB	Q9v233 pyrococcus
35	34	474	1 MPPA_BLAEM	P97997 blastoclad
36	34	529	1 RADA_PYRHO	O58001 pyrococcus
37	34	633	1 DXS_BACSU	P54523 bacillus su
38	34	637	1 PBPA_STORR	Q00573 streptococc
39	33	66	1 RS27_SULTO	Q973f9 sulfolobus
40	33	107	1 THIO_STRLC	Q05739 streptomyce
41	33	195	1 PYRE_SULSO	Q9ux09 sulfolobus
42	33	249	1 YAT6_RHOBL	P05449 rhodopseudo
43	33	270	1 URED_SYNY3	P73047 synecocyst
44	33	306	1 OPRR_PSEAE	Q01610 pseudomonas
45	33	340	1 ADHA_RHIME	O31186 rhizobium m

## ALIGNMENTS

### RESULT 1

AC	RPIA_CHLMU	STANDARD;	PRT;	239 AA.
AD	O9PK10:			
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Ribose 5-phosphate isomerase A (EC 5.3.1.6)	(Phosphoriboisomerase A)		
DE	(PRI)			
GN	RPIA OR TC0485.			
OS	Chlamydia muridarum.			
OC	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.			
OX	NCBI_TaxID=83560;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MoPn / Ni99;			
RX	MEDLINE=20150255; PubMed=10684935;			
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,			
RA	White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,			
RA	Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,			
RA	Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,			
RA	Eisen J., Fraser C.M.;			
RT	'Genome sequences of Chlamydia trachomatis MoPn and Chlamydia			
RT	pneumoniae AR39.';			
RL	Nucleic Acids Res. 28:1397-1406(2000).			
CC	-!- CATALYTIC ACTIVITY: D-ribose 5-phosphate - D-ribose 5-phosphate.			
CC	-!- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.			
CC	-!- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.			
CC				
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CC				
CC	EMBL; AE002317; AAF39331.1; -			
DR	PIR; E81697; E81697.			
DR	TIGR; TC0485.			
DR	HAWAP; MF_00170; -; 1.			
DR	InterPro; IPR001034; HTH_Deor.			
DR	InterPro; IPR004788; Rpia.			
DR	Pfam; PF00455; Deor; 1.			
DR	ProDom; PD005813; Rpia; 1.			
KW	Isonerace; Complete proteome.			
SQ	SEQUENCE 239 AA; 26180 MW; CSAD56AFA682B3D37 CRC64;			

Query Match 59.1%; Score 39; DB 1; Length 239;

Best Local Similarity 66.7%; Pred. No. 4.9;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATLRYKGGGXA 13

Db 102 ANLRWKGCGGA 113

## RESULT 2

PE21\_MOUSE  
ID PE21\_MOUSE STANDARD; PRT; 405 AA.  
AC P35375;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE prostaglandin E2 receptor, EPI subtype (prostanoid EPI receptor) (PGE  
DE receptor, EPI subtype).  
GN PTGER1 OR PTGEREPI.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ddy; TISSUE=Kidney;  
RX MEDLINE=9338584; PubMed=7690750;  
RA Watabe A., Sugimoto Y., Honda A., Irie A., Namba T., Negishi M.,  
RA Ito S., Narumiya S., Ichikawa A.;  
RT "Cloning and expression of cDNA for a mouse EPI subtype of  
RT prostaglandin E receptor".  
RL J. Biol. Chem. 268:20175-20178(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RX MEDLINE=95377316; PubMed=7649181;  
RA Batschke B., Nilsson C., Sundelin J.;  
RA "Molecular characterization of the mouse prostanoid EPI receptor  
RT gene".  
RL Eur. J. Biochem. 231:809-814(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RX MEDLINE=97011095; PubMed=8858105;  
RA Batschke B., Sundelin J.;  
RT "The mouse genes for the EPI prostanoid receptor and the PKN protein  
RT kinase overlap".  
RL Biochem. Biophys. Res. Commun. 227:70-76(1996).  
CC -!- FUNCTION: RECEPTOR FOR PROSTAGLANDIN E2 (PGE2). THE ACTIVITY OF  
CC THIS RECEPTOR IS MEDIATED BY G-Q PROTEINS WHICH ACTIVATE A  
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. MAY PLAY A  
CC ROLE AS AN IMPORTANT MODULATOR OF RENAL FUNCTION. IMPLICATED THE  
CC SMOOTH MUSCLE CONTRACTILE RESPONSE TO PGE2 IN VARIOUS TISSUES.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: ABUNDANT IN KIDNEY AND IN A LESSER AMOUNT IN  
CC LUNG.  
CC -!- PTM: PHOSPHORYLATED (POTENTIAL).  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
CC EMBL; D16338; BAA03842.1; -  
CC EMBL; Z49987; CAA90278.1; -  
CC EMBL; Y07611; CAA68884.1; -  
CC PIR; S66525; S66525.  
CC MGD; MGI:97793; Ptger1.  
CC InterPro; IPR000276; GPCR\_rhodpsn.  
CC Pfam; PF00001; 7tm\_1.1.  
CC PROSITE; PS00437; G\_PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE; PS00362; G\_PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Phosphorylation.  
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 40 62 1 (POTENTIAL).  
FT DOMAIN 63 80 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 81 99 2 (POTENTIAL).  
FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 114 135 3 (POTENTIAL).  
FT DOMAIN 136 157 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 158 179 4 (POTENTIAL).  
FT DOMAIN 180 202 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 203 228 5 (POTENTIAL).  
FT DOMAIN 229 301 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 302 323 6 (POTENTIAL).  
FT DOMAIN 324 337 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 338 357 7 (POTENTIAL).  
FT DOMAIN 358 405 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DISULFID 112 190 BY SIMILARITY.  
SQ SEQUENCE 405 AA; 42965 MW; 2B64DA21005CF8D6 CRC64;  
Query Match 57.6%; Score 38; DB 1; Length 405;  
Local Similarity 66.7%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 ATLRYKGGXA 13  
DB 277 ATLRSSRGSSA 288  
RESULT 3  
BACC\_BACLI  
ID BACC\_BACLI STANDARD; PRT; 6359 AA.  
AC 068008;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bacitracin synthetase 3 (BA3) [Includes: ATP-dependent Isoleucine  
DE adenylation (D-Phe) (Isoleucine activase); ATP-dependent Isoleucine  
DE adenylation (D-Phe) (D-phenylalanine activase); ATP-dependent histidine  
DE adenylation (HisA) (Histidine activase); ATP-dependent D-aspartate  
DE adenylation (D-AspA) (D-aspartate activase); ATP-dependent asparagine  
DE adenylation (AsnA) (Asparagine activase); Aspartate racemase  
DE (EC 5.1.1.13); Phenylalanine racemase [ATP hydrolyzing]  
DE (EC 5.1.1.11)].  
GN BACC.  
OS Bacillus licheniformis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1402;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 10716;  
RX MEDLINE=98089193; PubMed=9427658;  
RA Konz D., Klenz A., Schoergendorfer K., Marahiel M.A.;  
RT "The bacitracin biosynthesis operon of Bacillus licheniformis ATCC  
RT 10716: molecular characterization of three multi-modular peptide  
RT synthetases".  
RL Chem. Biol. 4:927-937(1997).  
CC -!- FUNCTION: INDUCES PEPTIDE SYNTHESIS, ACTIVATES AND INCORPORATES  
CC FIVE AMINO ACIDS, FORMS A THIAZOLINE RING BETWEEN THE FIRST TWO  
CC AMINO ACIDS AND INCORPORATES A D-GLUTAMINE IN THE FOURTH POSITION.  
CC -!- CATALYTIC ACTIVITY: L-aspartate -> D-aspartate.  
CC -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine -> AMP + diphosphate + D-  
CC phenylalanine.  
CC -!- COFACTOR: CONTAINS 5 COVALENTLY BOUND PHOSPHOPANTHETINES  
CC (POTENTIAL).  
CC -!- PATHWAY: Cyclic peptide antibiotic bacitracin biosynthesis.  
CC -!- SUBUNIT: LARGE MULTIMERIC COMPLEX OF BA1, BA2 AND BA3.  
CC -!- DOMAIN: CONSISTS OF FIVE MODULES WITH TWO EPIMERIZATION DOMAINS IN  
CC THE SECOND AND FOURTH MODULES, AND A PUTATIVE C-TERMINAL  
CC THIOESTERASE DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID INTO  
CC THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS  
CC RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION  
CC (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), AND  
CC N METHYLATION (OPTIONAL).  
CC -!- MISCELLANEOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC  
RC TISSUE=Brain;  
RX MEDLINE=99424063; PubMed=10231032;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XIII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 6:63-70(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC  
RC TISSUE=Testis;  
RX MEDLINE=21154917; PubMed=11230166;  
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,  
RA Ansorge W., Boecker M., Bloecher H., Bausachs S., Blum H.,  
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,  
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,  
RA Wambutt R., Korn B., Klein M., Poustka A.;  
RT "Towards a catalog of human genes and proteins: sequencing and  
RT analysis of 500 novel complete protein coding human cDNAs.";  
RL Genome Res. 11:422-435(2001).  
RN [3]  
RP IDENTIFICATION IN TRAPP COMPLEX.  
RC  
RX MEDLINE=21664186; PubMed=11805826;  
RA Gavin A.C., Bosche M., Krause R., Grandi P., Marzioch M., Bauer A.,  
RA Schultz J., Rick J.M., Michon A.M., Crutiat C.M., Remor M., Hofert C.,  
RA Schelder M., Rajkajovic M., Ruffner H., Merino A., Klein K., Hudak M.,  
RA Dickson D., Rudi T., Gnaul V., Bauch A., Bastuck S., Huhse B.,  
RA Leutwein C., Heurter M.A., Copley R.R., Edelmann A., Querfurth E.,  
RA Rybin V., Drewes G., Raida M., Boumeester T., Bork P., Seraphin B.,  
RA Kuster B., Neubauer G., Superti-Furga G.;  
RT "Functional organization of the yeast proteome by systematic analysis  
RT of protein complexes.";  
RL Nature 415:141-147(2002).  
RN [4]  
RP -1- FUNCTION: May play role in vesicular transport from endoplasmic  
RC reticulum to Golgi.  
CC  
CC -1- SUBUNIT: Part of the multisubunit TRAPP (transport protein  
CC particle) complex.  
CC  
CC -1- SUBCELLULAR LOCATION: Cis-Golgi complex (By similarity).  
CC  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9Y2L5-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9Y2L5-2; Sequence=VSP\_004000;  
CC Note=No experimental confirmation available;  
CC  
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CC  
CC EMBL; AB023329; BAA76856.1; -  
CC EMBL; AL136749; CAB66683.1; -  
DR GO: GO:0005801; C:Golgi cis-face; NAS.  
DR GO: GO:0005478; F:Intracellular transport; NAS.  
DR GO: GO:0006888; P:ER to Golgi transport; NAS.  
KW Transport; Endoplasmic reticulum; Golgi stack; Alternative splicing.  
FT VARSPLIC 916 1002 Missing (in isoform 2).  
FT FTID=VSP\_004000.  
FT CONFLICT 251 251 K -> E (IN REF. 2).  
FT CONFLICT 1146 1146 A -> T (IN REF. 2).  
SQ SEQUENCE 1435 AA; 160940 MW; 35C7C96BCE422B04 CRC64;  
Query Match 56.1%; Score 37; DB 1; Length 1435;

Best Local Similarity	54.5%	Pred. NO. 75;	Matches	6;	Conservative	2;	Mismatches	3;	Indels	0;	Gaps	0;
QY	1	CATLVRYKGG 11										
DB	585	COMQVYKGG 595										
RESULT 5												
INX4_DROME												
ID	INX4_DROME	STANDARD;	PRT;	367	AA.							
AC	Q9VRX6;											
DT	16-OCT-2001 (Rel. 40, Created)											
DT	16-OCT-2001 (Rel. 40, Last sequence update)											
DT	15-SEP-2003 (Rel. 42, Last annotation update)											
DE	Innexin INx4 (Innexin-4) (Zero population growth protein).											
GN	ZPG OR INX4 OR CG10125.											
OS	Drosophila melanogaster. (Fruit fly).											
OC	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;											
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;											
OC	Ephydroidea; Drosophilidae; Drosophila.											
OX	NCBI_Taxid=7227;											
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.											
RP	TISSUE-Ovary;											
RC	MEDLINE-21959302; PubMed-11960713;											
RX	Stebbins L.A., Todman M.G., Phillips R., Greer C.E., Tam J.,											
RX	Phelan P., Jacobs K., Bacon J.P., Davies J.A.;											
RT	"Gap junctions in Drosophila: developmental expression of the entire											
RT	Innexin gene family".											
RL	Mech. Dev. 113:197-205(2002).											
RN	[2]											
RP	SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE											
RP	SPECIFICITY, AND DEVELOPMENTAL STAGE.											
RC	TISSUE-Ovary;											
RX	PubMed-11973283;											
RX	Tazuke S.I., Schulz C., Gilboa L., Fogarty M., Mahowald A.P.,											
RA	Guichet A., Eshruski A., Wood C.G., Lehmann R., Fuller M.T.;											
RA	"A germline-specific gap junction protein required for survival of											
RT	differentiating early germ cells.";											
RL	Development 129:2529-2539(2002).											
RN	[3]											
RP	SEQUENCE FROM N.A.											
RC	STRAIN-Berkeley;											
RX	MEDLINE-20196006; PubMed-10731132;											
RX	Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,											
RA	Anatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,											
RA	Georgis R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,											
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,											
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,											
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,											
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,											

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RPIA_AGR5S
ID RPIA_AGR5S STANDARD; PRT; 231 AA.
AC Q92942; Q9JQ38;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
DE (PRI).
GN RPIA OR ATU1613 OR AGR_C_2972.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayvan T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Senphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Foo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao X., Astenzai M., Halling C., Mullin L.,
RA Houmel K., Gordon J., Vaudin D., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
CC -|- CATALYTIC ACTIVITY: D-ribose 5-phosphate -> D-ribulose 5-phosphate.
CC -|- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
CC -|- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; A6009118; AAL42615.1; ALU_INIT.
CC EMBL; A6008083; RAK87392.1;
CC PIR; G97554; G97554.
CC HAMAP; MF_00170; -.
CC InterPro; IPR001034; HTH_Deor.
CC InterPro; IPR004788; RpiA.
CC Pfam; PF00455; deor; 1.
CC ProDom; PD005813; RpiA; 1.
CC TIGRFAMs; TIGR00021; rpiA; 1.
CC Isomerase; Complete proteome.
KW Isomerase; Complete proteome.
SQ SEQUENCE 231 AA; 24140 MW; A209E2E2905C2CED CRC64;

Query Match 53.0%; Score 35; DB 1; Length 231;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRVYKGGGXA 13
||: |||||
DB 92 LRLVKGGGGA 101

RPIA_CHLPN
ID RPIA_CHLPN STANDARD; PRT; 231 AA.
AC Q92942; Q9JQ38;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
DE (PRI).
GN RPIA OR CPN0141 OR CP0631.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA."
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -|- CATALYTIC ACTIVITY: D-ribose 5-phosphate -> D-ribulose 5-phosphate.
CC -|- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
CC -|- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
CC
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CC
CC EMBL; A6001600; AAD18294.1;
CC EMBL; A6002221; AAF38446.1;
CC EMBL; A6002545; BAA98351.1;
CC PIR; B72115; B72115.
CC PIR; E86508; E86508.
CC TIGR; CP0631; -.
CC HAMAP; MF_00170; -.
CC InterPro; IPR004788; RpiA.
CC ProDom; PD005813; RpiA; 1.
CC Isomerase; Complete proteome.
KW Isomerase; Complete proteome.
SQ SEQUENCE 231 AA; 25574 MW; C2DD9CFF6F370C17 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 231;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LRVYKGGGXA 13
||: |||||
DB 92 LRLVKGGGGA 101

```

Db 96 LRMIKGGGA 105

RESULT 8

RPIA\_RHIME STANDARD; PRT; 231 AA.

AC Q92PB8; 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A) (PRI).

GN RPIA OR R01856 OR SMC00152.

OS Rhizobium meliloti (Sinorhizobium meliloti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.

OX NCBI\_TaxID=382;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1021;

RX MEDLINE=21396507; PubMed=11481430;

RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Bostard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;

RA 'Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.';

RT Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

RL -|- CATALYTIC ACTIVITY: D-ribose 5-phosphate -> D-ribulose 5-phosphate.

CC -|- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.

CC -|- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.

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DR EMBL; AL591788; CAC46435.1; 1.

DR HAMAP; MF\_00170; 1.

DR InterPro; IPR001034; HTH\_Deor.

DR InterPro; IPR004788; RPIA.

DR Pfam; PF00455; deor; 1.

DR ProDom; PD005813; RPIA; 1.

DR TIGRFAMs; TIGR00021; rpiA; 1.

KW Isomerase; Complete proteome.

SQ SEQUENCE 231 AA; 24054 MW; 461B9638D4E9C448 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 231;

Best Local Similarity 70.0%; Pred. NO. 26;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 LRVYKGGGA 13

DB 92 LRLKGGGA 101

RESULT 9

RPIA\_METAC STANDARD; PRT; 234 AA.

AC Q8TQ69; 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A) (PRI).

GN RPIA OR M1683.

OS Methanosarcina acetivorans.

OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;

OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.

OX NCBI\_TaxID=2214;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C2A / ATCC 35395 / DSM 2834;

RX MEDLINE=21929760; PubMed=1193238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas D.E., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B.;

RA 'The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.';

RL Genome Res. 12:532-542(2002).

CC -|- CATALYTIC ACTIVITY: D-ribose 5-phosphate -> D-ribulose 5-phosphate.

CC -|- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.

CC -|- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.

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DR EMBL; AE010842; AM05090.1; 1.

DR HAMAP; MF\_00170; 1.

DR InterPro; IPR004788; RPIA.

DR ProDom; PD005813; RPIA; 1.

DR TIGRFAMs; TIGR00021; rpiA; 1.

KW Isomerase; Complete proteome.

SQ SEQUENCE 234 AA; 24940 MW; 7CCDD8FE179FE5D0 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 234;

Best Local Similarity 70.0%; Pred. NO. 27;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 LRVYKGGGA 13

DB 99 LRAIKGGGA 108

RESULT 10

RPIA\_CHLTR STANDARD; PRT; 242 AA.

AC O84215; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A) (PRI).

GN RPIA OR CT213.

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI\_TaxID=813;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=D/UW-3/Cx;

RX MEDLINE=99000809; PubMed=9784136;

RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;

RA 'Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.';

RL Science 282:754-759(1998).

CC -|- CATALYTIC ACTIVITY: D-ribose 5-phosphate -> D-ribulose 5-phosphate.

CC -|- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.

CC -1- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.  
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 CC -----  
 DR EMBL; AF001295; AAC67805.1; -  
 DR PIR; D71542; D71542.  
 DR HAMAP; MF\_00170; -; 1.  
 DR InterPro; IPR001034; HTH\_Deor.  
 DR InterPro; IPR004788; RpiA.  
 DR Pfam; PF00455; deor; 1.  
 DR ProDom; PD005813; RpiA; 1.  
 KW Isomerase; Complete proteome.  
 SQ SEQUENCE 242 AA; 26646 MW; D59C38284D2229B2 CRC64;  
 Query Match 53.0%; Score 35; DB 1; Length 242;  
 Best Local Similarity 70.0%; Pred. No. 28;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 LRVYKGGXA 13  
 II: ||||| I  
 DB 104 LRVYKGGGA 113  
 RESULT 11  
 PHOS\_MOUSE  
 ID PHOS\_MOUSE STANDARD; PRT; 244 AA.  
 AC Q9QW08;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Phosducin (PHD) (33 kDa phototransducing protein) (Rod photoreceptor  
 DE 1) (RPR-1).  
 DE PDC OR RPRI.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Retina;  
 RX MEDLINE=94009395; PubMed=8405193;  
 RA Groshan K.R., Norton J.C., Craft C.M., Travis G.H.;  
 RT "Isolation and characterization of a cDNA for mouse retinal  
 RT phosducin".  
 RL Exp. Eye Res. 57:253-255(1993).  
 CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL  
 CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR  
 CC METABOLISM.  
 CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of  
 CC the GTP-binding protein, transducin.  
 CC -1- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.  
 CC -1- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS  
 CC MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; L08075; AAK13559.1; -  
 DR PIR; JC2018; JC2018.  
 DR HSP; P20942; IB9X.  
 DR MGD; MGI:98090; Pdc.

DR InterPro; IPR001200; Phosducin.  
 DR InterPro; IPR006663; Thioresox\_dom2.  
 DR Pfam; PF02114; Phosducin; 1.  
 DR PRINTS; PR00677; PHOSDUCIN.  
 KW Vision; Sensory transduction; Phosphorylation.  
 CC MOD\_RES 71 71 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).  
 SQ SEQUENCE 244 AA; 28016 MW; F42361EA25F0F254 CRC64;  
 Query Match 53.0%; Score 35; DB 1; Length 244;  
 Best Local Similarity 87.5%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TLRVYKGG 10  
 II: |||||  
 DB 186 TLRVYKGG 193  
 RESULT 12  
 PHOS\_BOVIN  
 ID PHOS\_BOVIN STANDARD; PRT; 245 AA.  
 AC P19632; P20940; Q28160;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein).  
 DE PDC.  
 GN Bos taurus (Bovine).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE, AND SEQUENCE OF 228-245 FROM N.A.  
 RC TISSUE=Retina;  
 RX MEDLINE=90368806; PubMed=2203790;  
 RA Lee R.H., Fowler A., McGinnis J.F., Lolley R.N., Craft C.M.;  
 RT "Amino acid and cDNA sequence of bovine phosducin, a soluble  
 RT phosphoprotein from photoreceptor cells".  
 RL J. Biol. Chem. 265:15867-15873(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89364083; PubMed=2770450;  
 RA Kuo C.-H., Akiyama M., Miki N.;  
 RT "Isolation of a novel retina-specific clone (MEKA cDNA) encoding a  
 RT photoreceptor soluble protein".  
 RL Brain Res. Mol. Brain Res. 6:1-10(1989).  
 RN [3]  
 RP SEQUENCE OF 8-245 FROM N.A.  
 RC TISSUE=Pinel gland, and Retina;  
 RX MEDLINE=91007277; PubMed=2210381;  
 RA Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,  
 RA Shinohara T.;  
 RT "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in  
 RT retina and pineal gland".  
 RL Gene 91:209-215(1990).  
 RN [4]  
 RP PHOSPHORYLATION OF SER-73.  
 RX MEDLINE=90368805; PubMed=2394752;  
 RA Lee R.H., Brown B.M., Lolley R.N.;  
 RT "Protein kinase A phosphorylates retinal phosducin on serine 73 in  
 RT situ".  
 RL J. Biol. Chem. 265:15860-15866(1990).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH G-BETA AND  
 RP G-GAMMA.  
 RX MEDLINE=98416696; PubMed=9739091;  
 RA Loew A., Ho Y.K., Blundell T., Bax B.;  
 RT "Phosducin induces a structural change in transducin beta gamma.";  
 RL Structure 6:1007-1019(1998).  
 CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL  
 CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR  
 CC METABOLISM.  
 CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of

the GTP-binding protein, transducin.  
 -|- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.  
 -|- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS  
 MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.  
 -|- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.  
 -|- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS  
 DUE TO A FRAMESHIFT.

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 EMBL; M58170; AAA62116.1; -;  
 EMBL; M33529; AAA30349.1; -;  
 PIR; A38379; A38379.  
 PDB; 1A0R; 16-FEB-99.  
 InterPro; IPR001200; Phosducin.  
 InterPro; IPR006663; Thioresox\_dom2.  
 Pfam; PF01114; Phosducin; 1.  
 PRINTS; PR00677; PHOSDUCIN.  
 Vision; Sensory transduction; Phosphorylation; 3D-structure.  
 MOD\_RES 73 73 PHOSPHORYLATION (BY PKA).  
 CONFLICT 44 44 H -> P (IN REF. 3).  
 CONFLICT 238 239 TN -> SK (IN REF. 3).  
 HELIX 21 35  
 TURN 36 36  
 HELIX 74 80  
 TURN 81 82  
 HELIX 87 105  
 STRAND 114 116  
 HELIX 120 128  
 TURN 132 133  
 STRAND 135 141  
 TURN 143 144  
 TURN 146 147  
 HELIX 148 161  
 TURN 163 164  
 STRAND 166 171  
 HELIX 172 175  
 TURN 178 179  
 TURN 183 185  
 STRAND 188 193  
 TURN 194 195  
 STRAND 196 201  
 TURN 202 203  
 HELIX 204 207  
 TURN 210 211  
 HELIX 214 222  
 TURN 223 225  
 SEQUENCE 245 AA; 28231 MW; 5CA621610401D550 CRC64;  
 Query Match 53.0%; Score 35; DB 1; Length 245;  
 Best Local Similarity 87.5%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TLRYVKGK 10  
 || |||||  
 Db 188 TLLVYKGG 195

RESULT 13  
 PHOS\_FELCA  
 ID PHOS\_FELCA STANDARD; PRT; 245 AA.  
 AC P41686;  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosducin (PHD) (33 kDa phototransducing protein).  
 GN PDC.

OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Abysinnian; TISSUE=Retina;  
 RX MEDLINE=95178554; PubMed=7873608;  
 RA Gorin M.B., To A.C., Narfstrom K.;  
 RT "Sequence analysis and exclusion of phosducin as the gene for the  
 recessive retinal degeneration of the Abyssinian cat.";  
 RL Biochim. Biophys. Acta 1260:323-327(1995).  
 CC -|- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL  
 PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR  
 METABOLISM.  
 CC -|- SUBUNIT: Forms a complex with the beta and gamma subunits of  
 the GTP-binding protein, transducin.  
 CC -|- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS  
 (BY SIMILARITY).  
 CC -|- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.  
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 EMBL; L35314; AAB59257.1; -;  
 PIR; S52096; S52096.  
 HSP; P20942; 1B9X.  
 InterPro; IPR001200; Phosducin.  
 InterPro; IPR006663; Thioresox\_dom2.  
 Pfam; PF01114; Phosducin; 1.  
 PRINTS; PR00677; PHOSDUCIN.  
 Vision; Sensory transduction; Phosphorylation.  
 MOD\_RES 73 73 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).  
 SEQUENCE 245 AA; 28363 MW; 9807CD30C32F8B21 CRC64;  
 Query Match 53.0%; Score 35; DB 1; Length 245;  
 Best Local Similarity 87.5%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TLRYVKGK 10  
 || |||||  
 Db 188 TLLVYKGG 195

RESULT 14  
 PHOS\_RAT  
 ID PHOS\_RAT STANDARD; PRT; 246 AA.  
 AC P20942; Q63420;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein) (Rod  
 photoreceptor 1) (RPR-1).  
 GN PDC OR RPRI.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Pineal gland, and Retina;  
 RX MEDLINE=91007277; PubMed=2210381;  
 RA Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,  
 RA Shinohara T.;  
 RT "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in  
 retina and pineal gland.";  
 RL Gene 91:209-215(1990).  
 RN [2]



SEQUENCE FROM N.A.  
 TISSUE-Pineal gland;  
 MEDLINE-91301696; PubMed-20711146;  
 RA Craft C.M., Lolley R.N., Seldin M.F., Lee R.H.;  
 "Rat pineal gland phosducin: cDNA isolation, nucleotide sequence, and  
 RT chromosomal assignment in the mouse.";  
 RL Genomics 10:400-409(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH G-BETA AND  
 RP G-GAMMA.  
 RX MEDLINE-99288453; PubMed-10360181;  
 RA Gaudet R., Savage J.R., McLaughlin J.N., Willardson B.M., Sigler P.B.;  
 "A molecular mechanism for the phosphorylation-dependent regulation of  
 RT heterotrimeric G-proteins by phosducin. Structural analysis of  
 RT phosducin and its phosphorylation-regulated interaction with  
 RT transducin beta-gamma.";  
 RL Mol. Cell 3:649-660(1999).  
 CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL  
 CC METABOLISM.  
 CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of  
 CC the GTP-binding protein, transducin.  
 CC -1- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.  
 CC -1- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS  
 CC MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M33528; AAA40604.1; -;  
 DR EMBL; M33530; AAA40603.1; -;  
 DR EMBL; M60738; AAA41841.1; -;  
 DR PIR; A39903; A39903.  
 DR PIR; JH0216; JH0216.  
 DR PDB; 1B9X; 23-FEB-99.  
 DR PDB; 1B9Y; 23-FEB-99.  
 DR PDB; 2TRC; 05-JUN-97.  
 DR InterPro; IPR001200; Phosducin.  
 DR InterPro; IPR006663; Thioresox\_dom2.  
 DR Pfam; PF02114; Phosducin; 1.  
 DR PRINTS; PR00677; PHOSDUCIN.  
 DR Vision; Sensory transduction; Phosphorylation; 3D-structure.  
 DR MOD\_RES 73 73  
 DR VARIANT 191 191  
 DR CONFLICT 39 39  
 DR CONFLICT 88 88  
 DR CONFLICT 119 119  
 DR CONFLICT 211 211  
 DR HELIX 21 36  
 DR TURN 37 37  
 DR TURN 88 105  
 DR STRAND 114 116  
 DR TURN 120 128  
 DR TURN 132 133  
 DR STRAND 135 141  
 DR TURN 143 144  
 DR TURN 146 147  
 DR TURN 148 161  
 DR TURN 163 164  
 DR STRAND 166 171  
 DR TURN 172 175  
 DR TURN 176 176  
 DR TURN 178 180  
 DR TURN 183 185  
 DR STRAND 188 193  
 DR TURN 194 195  
 DR STRAND 196 201

FT TURN 202 203  
 FT HELIX 204 207  
 FT TURN 214 222  
 FT TURN 223 225  
 SQ SEQUENCE 246 AA; 28129 MW; 3C48ABCB4E5E3D04 CRC64;  
 Query Match 53.0%; Score 35; DB 1; Length 246;  
 Best Local Similarity 87.5%; Pred. NO. 28;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TLRVYKGG 10  
 DB 188 TLRVYKGG 195  
 RESULT 15  
 CFAA\_BACUT STANDARD; PRT; 340 AA.  
 ID CFAA\_BACUT  
 AC Q45729;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pesticidal crystal protein cry15aa (insecticidal delta-endotoxin  
 DE CryXVA(a)) (Crystalline entomocidal protoxin) (38 kDa crystal  
 DE protein).  
 GN CRY15AA OR CRYXVA(A).  
 OS Bacillus thuringiensis (subsp. thompsoni).  
 OG Plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_Taxid=44162;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92105024; PubMed-1729243;  
 RA Brown K.L., Whiteley H.R.;  
 RT Molecular characterization of two novel crystal protein genes from  
 RT Bacillus thuringiensis subsp. thompsoni.";  
 RL J. Bacteriol. 174:549-557(1992).  
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE.  
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
 CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
 CC OF THE SPORE COAT.  
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 CC -----  
 DR EMBL; M76442; AAA22333.1; -;  
 DR PIR; B41969; B41969.  
 DR InterPro; IPR005831; Aer\_hem.  
 KW Toxin; Sporulation; Plasmid.  
 SQ SEQUENCE 340 AA; 37547 MW; BCBFA2A2FE9B1FA50 CRC64;  
 Query Match 53.0%; Score 35; DB 1; Length 340;  
 Best Local Similarity 75.0%; Pred. NO. 40;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ATLRYVYKGG 9  
 DB 160 ATLQIVYKGG 167

Search completed: August 28, 2003, 18:35:12  
 Job time : 8.69697 secs